

SEQUENCE LISTING

5 <110> Degussa AG

<120> Process for the preparation of L-amino acids using strains
of the Enterobacteriaceae family

10 <130> 020479 BT

15 <160> 4

<170> PatentIn version 3.1

20 <210> 1
<211> 31
<212> DNA
<213> Artificial sequence

25 <220>
<221> Primer
<222> (1)..(31)
30 <223> eno1

<400> 1
gtttgtctag agtttcagtt taactagtga c 31

35 <210> 2
<211> 25
<212> DNA
<213> Artificial sequence

40 <220>
<221> Primer
<222> (1)..(25)
45 <223> eno2

<400> 2 25
ccggaggctg gcaagcttaa atcag

50 <210> 3
<211> 1381
<212> DNA
<213> Escherichia coli

55 <220>
<221> PCR product
<222> (1)..(1381)
60 <223>

<220>
<221> CDS

<222> (46)..(1344)

<223> eno gene

5 <400> 3

```

gtttgtctag agtttcagtt taactagtga cttgaggaaa accta atg tcc aaa atc      57
                                     Met Ser Lys Ile
                                     1
10  gta aaa atc atc ggt cgt gaa atc atc gac tcc cgt ggt aac ccg act      105
    Val Lys Ile Ile Gly Arg Glu Ile Ile Asp Ser Arg Gly Asn Pro Thr
    5                               10                               15                               20
15  gtt gaa gcc gaa gta cat ctg gag ggt ggt ttc gtc ggt atg gca gct      153
    Val Glu Ala Glu Val His Leu Glu Gly Gly Phe Val Gly Met Ala Ala
                                25                               30                               35
20  gct ccg tca ggt gct tct act ggt tcc cgt gaa gct ctg gaa ctg cgc      201
    Ala Pro Ser Gly Ala Ser Thr Gly Ser Arg Glu Ala Leu Glu Leu Arg
                                40                               45                               50
25  gat ggc gac aaa tcc cgt ttc ctg ggt aaa ggc gta acc aaa gct gtt      249
    Asp Gly Asp Lys Ser Arg Phe Leu Gly Lys Gly Val Thr Lys Ala Val
                                55                               60                               65
30  gct gcg gta aac ggc ccg atc gct cag gcg ctg att ggc aaa gat gct      297
    Ala Ala Val Asn Gly Pro Ile Ala Gln Ala Leu Ile Gly Lys Asp Ala
    70                               75                               80
35  aaa gat cag gct ggc att gac aag atc atg atc gac ctg gac ggc acc      345
    Lys Asp Gln Ala Gly Ile Asp Lys Ile Met Ile Asp Leu Asp Gly Thr
    85                               90                               95                               100
40  gaa aac aaa tcc aaa ttc ggc gcg aac gca atc ctg gct gta tct ctg      393
    Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Ala Val Ser Leu
                                105                               110                               115
45  gct aac gcc aaa gct gct gca gct gct aaa ggt atg ccg ctg tac gag      441
    Ala Asn Ala Lys Ala Ala Ala Ala Lys Gly Met Pro Leu Tyr Glu
                                120                               125                               130
50  cac atc gct gaa ctg aac ggt act ccg ggc aaa tac tct atg ccg gtt      489
    His Ile Ala Glu Leu Asn Gly Thr Pro Gly Lys Tyr Ser Met Pro Val
                                135                               140                               145
55  ccg atg atg aac atc atc aac ggt ggt gag cac gct gac aac aac gtt      537
    Pro Met Met Asn Ile Ile Asn Gly Gly Glu His Ala Asp Asn Asn Val
    150                               155                               160
60  gat atc cag gaa ttc atg att cag ccg gtt ggc gcg aaa act gtg aaa      585
    Asp Ile Gln Glu Phe Met Ile Gln Pro Val Gly Ala Lys Thr Val Lys
    165                               170                               175                               180
65  gaa gcc atc cgc atg ggt tct gaa gtt ttc cat cac ctg gca aaa gtt      633
    Glu Ala Ile Arg Met Gly Ser Glu Val Phe His His Leu Ala Lys Val
                                185                               190                               195
70  ctg aaa gcg aaa ggc atg aac act gct gtt ggt gac gaa ggt ggc tat      681
    Leu Lys Ala Lys Gly Met Asn Thr Ala Val Gly Asp Glu Gly Gly Tyr
                                200                               205                               210
75  gcg ccg aac ctg ggt tcc aac gct gaa gct ctg gct gtt atc gct gaa      729
    Ala Pro Asn Leu Gly Ser Asn Ala Glu Ala Leu Ala Val Ile Ala Glu
    215                               220                               225

```

gct gtt aaa gct gct ggt tat gaa ctg ggc aaa gac atc act ttg gcg 777
 Ala Val Lys Ala Ala Gly Tyr Glu Leu Gly Lys Asp Ile Thr Leu Ala
 230 235 240

5 atg gac tgc gca gct tct gaa ttc tac aaa gat ggt aaa tac gtt ctg 825
 Met Asp Cys Ala Ala Ser Glu Phe Tyr Lys Asp Gly Lys Tyr Val Leu
 245 250 255 260

10 gct ggc gaa ggc aac aaa gcg ttc acc tct gaa gaa ttc act cac ttc 873
 Ala Gly Glu Gly Asn Lys Ala Phe Thr Ser Glu Glu Phe Thr His Phe
 265 270 275

15 ctg gaa gaa ctg acc aaa cag tac ccg atc gtt tct atc gaa gac ggt 921
 Leu Glu Glu Leu Thr Lys Gln Tyr Pro Ile Val Ser Ile Glu Asp Gly
 280 285 290

20 ctg gac gaa tct gac tgg gac ggt ttc gca tac cag acc aaa gtt ctg 969
 Leu Asp Glu Ser Asp Trp Asp Gly Phe Ala Tyr Gln Thr Lys Val Leu
 295 300 305

25 ggc gac aaa atc cag ctg gtt ggt gac gac ctg ttc gta acc aac acc 1017
 Gly Asp Lys Ile Gln Leu Val Gly Asp Asp Leu Phe Val Thr Asn Thr
 310 315 320

30 aag atc ctg aaa gaa ggt atc gaa aaa ggt atc gct aac tcc atc ctg 1065
 Lys Ile Leu Lys Glu Gly Ile Glu Lys Gly Ile Ala Asn Ser Ile Leu
 325 330 335 340

35 atc aaa ttc aac cag atc ggt tct ctg acc gaa act ctg gct gca atc 1113
 Ile Lys Phe Asn Gln Ile Gly Ser Leu Thr Glu Thr Leu Ala Ala Ile
 345 350 355

40 aag atg gcg aaa gat gct ggc tac act gca gtt atc tct cac cgt tct 1161
 Lys Met Ala Lys Asp Ala Gly Tyr Thr Ala Val Ile Ser His Arg Ser
 360 365 370

45 ggc gaa act gaa gac gct acc atc gct gac ctg gct gtt ggt act gct 1209
 Gly Glu Thr Glu Asp Ala Thr Ile Ala Asp Leu Ala Val Gly Thr Ala
 375 380 385

50 gca ggc cag atc aaa act ggt tct atg agc cgt tct gac cgt gtt gct 1257
 Ala Gly Gln Ile Lys Thr Gly Ser Met Ser Arg Ser Asp Arg Val Ala
 390 395 400

55 aaa tac aac cag ctg att cgt atc gaa gaa gct ctg ggc gaa aaa gca 1305
 Lys Tyr Asn Gln Leu Ile Arg Ile Glu Glu Ala Leu Gly Glu Lys Ala
 405 410 415 420

60 ccg tac aac ggt cgt aaa gag atc aaa ggc cag gca taa gactgacttt 1354
 Pro Tyr Asn Gly Arg Lys Glu Ile Lys Gly Gln Ala
 425 430

atctgattta agcttgccag cctccgg 1381

<210> 4
 <211> 432
 <212> PRT
 <213> Escherichia coli

<400> 4
 Met Ser Lys Ile Val Lys Ile Ile Gly Arg Glu Ile Ile Asp Ser Arg
 1 5 10 15

Gly Asn Pro Thr Val Glu Ala Glu Val His Leu Glu Gly Gly Phe Val
 20 25 30
 5 Gly Met Ala Ala Ala Pro Ser Gly Ala Ser Thr Gly Ser Arg Glu Ala
 35 40 45
 Leu Glu Leu Arg Asp Gly Asp Lys Ser Arg Phe Leu Gly Lys Gly Val
 50 55 60
 10 Thr Lys Ala Val Ala Ala Val Asn Gly Pro Ile Ala Gln Ala Leu Ile
 65 70 75 80
 15 Gly Lys Asp Ala Lys Asp Gln Ala Gly Ile Asp Lys Ile Met Ile Asp
 85 90 95
 Leu Asp Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu
 100 105 110
 20 Ala Val Ser Leu Ala Asn Ala Lys Ala Ala Ala Ala Lys Gly Met
 115 120 125
 Pro Leu Tyr Glu His Ile Ala Glu Leu Asn Gly Thr Pro Gly Lys Tyr
 130 135 140
 25 Ser Met Pro Val Pro Met Met Asn Ile Ile Asn Gly Gly Glu His Ala
 145 150 155 160
 30 Asp Asn Asn Val Asp Ile Gln Glu Phe Met Ile Gln Pro Val Gly Ala
 165 170 175
 Lys Thr Val Lys Glu Ala Ile Arg Met Gly Ser Glu Val Phe His His
 180 185 190
 35 Leu Ala Lys Val Leu Lys Ala Lys Gly Met Asn Thr Ala Val Gly Asp
 195 200 205
 Glu Gly Gly Tyr Ala Pro Asn Leu Gly Ser Asn Ala Glu Ala Leu Ala
 210 215 220
 40 Val Ile Ala Glu Ala Val Lys Ala Ala Gly Tyr Glu Leu Gly Lys Asp
 225 230 235 240
 45 Ile Thr Leu Ala Met Asp Cys Ala Ala Ser Glu Phe Tyr Lys Asp Gly
 245 250 255
 Lys Tyr Val Leu Ala Gly Glu Gly Asn Lys Ala Phe Thr Ser Glu Glu
 260 265 270
 50 Phe Thr His Phe Leu Glu Glu Leu Thr Lys Gln Tyr Pro Ile Val Ser
 275 280 285
 Ile Glu Asp Gly Leu Asp Glu Ser Asp Trp Asp Gly Phe Ala Tyr Gln
 290 295 300
 55 Thr Lys Val Leu Gly Asp Lys Ile Gln Leu Val Gly Asp Asp Leu Phe
 305 310 315 320
 60 Val Thr Asn Thr Lys Ile Leu Lys Glu Gly Ile Glu Lys Gly Ile Ala
 325 330 335
 Asn Ser Ile Leu Ile Lys Phe Asn Gln Ile Gly Ser Leu Thr Glu Thr
 340 345 350

Leu Ala Ala Ile Lys Met Ala Lys Asp Ala Gly Tyr Thr Ala Val Ile
355 360 365

5 Ser His Arg Ser Gly Glu Thr Glu Asp Ala Thr Ile Ala Asp Leu Ala
370 375 380

Val Gly Thr Ala Ala Gly Gln Ile Lys Thr Gly Ser Met Ser Arg Ser
385 390 395 400

10 Asp Arg Val Ala Lys Tyr Asn Gln Leu Ile Arg Ile Glu Glu Ala Leu
405 410 415

Gly Glu Lys Ala Pro Tyr Asn Gly Arg Lys Glu Ile Lys Gly Gln Ala
420 425 430